

#2 OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/854,326

DATE: 06/01/2001

TIME: 12:59:52

Input Set : A:\seqlist.txt

Output Set: C:\CRF3\06012001\I854326.raw

ENTERED

4 <110> APPLICANT: Toni R. Prezant (Inventor)  
 5 Shlomo Melmed (Inventor)  
 6 Anthony P. Heaney (Inventor)  
 12 <120> TITLE OF INVENTION: METHOD OF REGULATING BIOLOGICAL ACTIVITY  
 13 OF PITUITARY TUMOR TRANSFORMING GENE (PTTG)1 USING PTTG2  
 16 <130> FILE REFERENCE: 18810-81401  
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/854,326  
 19 <141> CURRENT FILING DATE: 2001-05-11  
 21 <150> PRIOR APPLICATION NUMBER: US09/730,469  
 22 <151> PRIOR FILING DATE: 2000-12-04  
 24 <150> PRIOR APPLICATION NUMBER: US 09/687,911  
 25 <151> PRIOR FILING DATE: 2000-10-13  
 27 <150> PRIOR APPLICATION NUMBER: US 09/569,956  
 28 <151> PRIOR FILING DATE: 2000-05-12  
 30 <150> PRIOR APPLICATION NUMBER: US 08/894,251  
 31 <151> PRIOR FILING DATE: 1999-07-23  
 33 <150> PRIOR APPLICATION NUMBER: PCT/US86/21463  
 34 <151> PRIOR FILING DATE: 1997-11-21  
 36 <150> PRIOR APPLICATION NUMBER: US 60/031,338  
 37 <151> PRIOR FILING DATE: 1996-11-21  
 39 <160> NUMBER OF SEQ ID NOS: 68  
 41 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 43 <210> SEQ ID NO: 1  
 44 <211> LENGTH: 974  
 45 <212> TYPE: DNA  
 46 <213> ORGANISM: Rattus rattus  
 48 <400> SEQUENCE: 1  
 49 aattcggcac gagccaacct tgagcatctg atcctcttgg cttctccttc ctatcgctga 60  
 50 gctggtaggc tggagacagt tggttgggtg ccaacatcaa caaacgattt ctgtagttta 120  
 51 gcgtttatga ccctggcggtg aagattttaag gtctggatta agcctgttga cttctccagc 180  
 52 tacttctaaa tttttgtgca taggtgctct ggtctctgtt gctgcttagt tcttccagcc 240  
 53 ttcctcaatg ccagttttat aatatgcagg tctctcccct cagtaatcca ggatggctac 300  
 54 tctgatcttt gtgataaagg ataacgaaga gccaggcagc cgtttggcat ctaaggatgg 360  
 55 attgaagctg ggcctcggtg tcaaaagcctt agatgggaaa ttgcaggttt caacgccacg 420  
 56 agtcggcaaa gtgttcggtg ccccaggcctt gcctaaagcc agcaggaagg ctctgggaac 480  
 57 tgtcaacaga gttactgaaa agccagtgaag gagtagtaaa cccctgcaat cgaaacagcc 540  
 58 gactctgagt gtgaaaaaga tcaccgagaa gtctactaag acacaaggct ctgctcctgc 600  
 59 tctcgatgat gcctaccagc aaatagaaaa gttcttcccc ttgatccctc tagattttga 660  
 60 gagttttgac ctgcctgaag agcaccagat ctcaactctc cccttgaatg gagtgcctct 720  
 61 catgatcctg aatgaagaga gggggcctga gaagctgctg cacctggacc ccccttcccc 780  
 62 tctgcagaag ccccttctac cgtgggaatc tgatccgttg ccgtctctc ccagcgccct 840  
 63 ctccgctctg gatgttgaat tgccgcctgt ttgttacgat gcagatatat aaacgtctta 900  
 64 ctctcttata gtttatgtaa gttgtattaa taaagcattt gtgtgtaaaa aaaaaaaaaa 960  
 65 aaactcgaga gtac 974  
 67 <210> SEQ ID NO: 2  
 68 <211> LENGTH: 199  
 69 <212> TYPE: PRT

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70 <213> ORGANISM: Rattus rattus
72 <400> SEQUENCE: 2
73 Met Ala Thr Leu Ile Phe Val Asp Lys Asp Asn Glu Glu Pro Gly Ser
74 1 5 10 15
75 Arg Leu Ala Ser Lys Asp Gly Leu Lys Leu Gly Ser Gly Val Lys Ala
76 20 25 30
77 Leu Asp Gly Lys Leu Gln Val Ser Thr Pro Arg Val Gly Lys Val Phe
78 35 40 45
79 Gly Ala Pro Gly Leu Pro Lys Ala Ser Arg Lys Ala Leu Gly Thr Val
80 50 55 60
81 Asn Arg Val Thr Glu Lys Pro Val Lys Ser Ser Lys Pro Leu Gln Ser
82 65 70 75 80
83 Lys Gln Pro Thr Leu Ser Val Lys Lys Ile Thr Glu Lys Ser Thr Lys
84 85 90 95
85 Thr Gln Gly Ser Ala Pro Ala Pro Asp Ala Tyr Pro Glu Ile Glu
86 100 105 110
87 Lys Phe Phe Pro Phe Asp Pro Leu Asp Phe Glu Ser Phe Asp Leu Pro
88 115 120 125
89 Glu Glu His Gln Ile Ser Leu Leu Pro Leu Asn Gly Val Pro Leu Met
90 130 135 140
91 Ile Leu Asn Glu Glu Arg Gly Leu Glu Lys Leu Leu His Leu Asp Pro
92 145 150 155 160
93 Pro Ser Pro Leu Gln Lys Pro Phe Leu Pro Trp Glu Ser Asp Pro Leu
94 165 170 175
95 Pro Ser Pro Pro Ser Ala Leu Ser Ala Leu Asp Val Glu Leu Pro Pro
96 180 185 190
97 Val Cys Tyr Asp Ala Asp Ile
98 195
101 <210> SEQ ID NO: 3
102 <211> LENGTH: 779
103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <400> SEQUENCE: 3
107 atggccgcga gttgtggttt aaaccaggag tgccgcgcgt cegttcaccc cggcctcaga 60
108 tgaatgcggc tgtaagacc tgcaataatc cagaatggct actctgatct atgttgataa 120
109 ggaataatgga gaaccaggca cccgtgtggt tgctaaggat gggctgaagc tggggctctg 180
110 accttcaatc aaagccttag atgggagatc tcaagtttca acaccacgtt ttggcaaaac 240
111 gttcgatgcc ccaccagcct tacctaaagc tactagaaag gctttgggaa ctgtcaacag 300
112 agctacagaa aagtctgtaa agaccaaggg acccctcaaa caaaaacagc caagcttttc 360
113 tgccaaaaag atgactgaga agactgttaa agcaaaaagc tctgttccgt cctcagatga 420
114 tgccctatcca gaaatagaaa aattctttcc cttcaatcct ctgacttttg agagttttga 480
115 cctgcctgaa gaggaccaga ttgcgcacct ccccttgagt ggagtgcctc tcatgatcct 540
116 tgacgaggag agagagcttg aaaagctgtt tcagctgggc ccccttcac ctgtgaagat 600
117 gccctctcca ccatgggaat ccaatctgtt gcagtctcct tcaagcattc tgtcgacct 660
118 ggatgttgaa ttgccacct tttgctgtga catagatatt taaatttctt agtgcttcag 720
119 agtttgtgtg tatttgtatt aataaagcat tctttaacag ataaaaaaaa aaaaaaaaaa 779
121 <210> SEQ ID NO: 4
122 <211> LENGTH: 202
123 <212> TYPE: PRT

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124 <213> ORGANISM: Homo sapiens
126 <400> SEQUENCE: 4
127 Met Ala Thr Leu Ile Tyr Val Asp Lys Glu Asn Gly Glu Pro Gly Thr
128 1 5 10 15
129 Arg Val Val Ala Lys Asp Gly Leu Lys Leu Gly Ser Gly Pro Ser Ile
130 20 25 30
131 Lys Ala Leu Asp Gly Arg Ser Gln Val Ser Thr Pro Arg Phe Gly Lys
132 35 40 45
133 Thr Phe Asp Ala Pro Pro Ala Leu Pro Lys Ala Thr Arg Lys Ala Leu
134 50 55 60
135 Gly Thr Val Asn Arg Ala Thr Glu Lys Ser Val Lys Thr Lys Gly Pro
136 65 70 75 80
137 Leu Lys Gln Lys Gln Pro Ser Phe Ser Ala Lys Lys Met Thr Glu Lys
138 85 90 95
139 Thr Val Lys Ala Lys Ser Ser Val Pro Ala Ser Asp Asp Ala Tyr Pro
140 100 105 110
141 Glu Ile Glu Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Glu Ser Phe
142 115 120 125
143 Asp Leu Pro Glu Glu His Gln Ile Ala His Leu Pro Leu Ser Gly Val
144 130 135 140
145 Pro Leu Met Ile Leu Asp Glu Glu Arg Glu Leu Glu Lys Leu Phe Gln
146 145 150 155 160
147 Leu Gly Pro Pro Ser Pro Val Lys Met Pro Ser Pro Pro Trp Glu Ser
148 165 170 175
149 Asn Leu Leu Gln Ser Pro Ser Ser Ile Leu Ser Thr Leu Asp Val Glu
150 180 185 190
151 Leu Pro Pro Val Cys Cys Asp Ile Asp Ile
152 195 200
155 <210> SEQ ID NO: 5
156 <211> LENGTH: 31
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Synthetic oligonucleotide.
163 <400> SEQUENCE: 5
164 gatgctctcc gcactctggg aatccaatct g 31
166 <210> SEQ ID NO: 6
167 <211> LENGTH: 32
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Synthetic oligonucleotide.
174 <400> SEQUENCE: 6
175 ttccacaagtt gaggggcgcc cagctgaaac ag 32
177 <210> SEQ ID NO: 7
178 <211> LENGTH: 32
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:

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```

183 <223> OTHER INFORMATION: Synthetic oligonucleotide specific to pCI-neo
184     plasmid. vector.
186 <400> SEQUENCE: 7
187 ggctagagta cttaatacga ctcactatag gc          32
189 <210> SEQ ID NO: 8
190 <211> LENGTH: 31
191 <212> TYPE: DNA
192 <213> ORGANISM: Homo sapiens
194 <400> SEQUENCE: 8
195 ctatgtcaca gcaaacaggt ggcaattcaa c          31
197 <210> SEQ ID NO: 9
198 <211> LENGTH: 56
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 9
203 Met Ile Leu Asp Glu Glu Arg Glu Leu Glu Lys Leu Phe Gln Leu Gly
204 1             5             10             15
205 Pro Pro Ser Pro Val Lys Met Pro Ser Pro Pro Trp Glu Ser Asn Leu
206             20             25             30
207 Leu Gln Ser Pro Ser Ser Ile Leu Ser Thr Leu Asp Val Glu Leu Pro
208             35             40             45
209 Pro Val Cys Cys Asp Ile Asp Ile
210             50             55
213 <210> SEQ ID NO: 10
214 <211> LENGTH: 168
215 <212> TYPE: DNA
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 10
219 atgataccttg acgaggagag agagcttgaa aagctgtttc agctggggccc cccttcacct 60
220 gtgaagatgc cctctccacc atgggaatcc aatctgttgc agtctccttc aagcattctg 120
221 tcgaccttgg atgttgaatt gccacctgtt tgctgtgaca tagatatt          168
223 <210> SEQ ID NO: 11
224 <211> LENGTH: 16
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Anchored primer sequence.
231 <400> SEQUENCE: 11
232 aagctttttt tttttg          16
234 <210> SEQ ID NO: 12
235 <211> LENGTH: 13
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Arbitrary primer sequence.
242 <400> SEQUENCE: 12
243 aagcttgctg etc          13
245 <210> SEQ ID NO: 13
246 <211> LENGTH: 16

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Input Set : A:\seqlist.txt  
 Output Set: C:\CRF3\06012001\I854326.raw

247 <212> TYPE: DNA  
 248 <213> ORGANISM: Artificial Sequence  
 250 <220> FEATURE:  
 251 <223> OTHER INFORMATION: n = a, g, or c; Anchored primer sequence.  
 253 <400> SEQUENCE: 13  
 W--> 254 aagctttttt tttttt 16  
 256 <210> SEQ ID NO: 14  
 257 <211> LENGTH: 194  
 258 <212> TYPE: PRT  
 259 <213> ORGANISM: Mus musculus  
 261 <400> SEQUENCE: 14  
 262 Met Ala Thr Leu Ile Phe Val Asp Lys Asp Asn Glu Glu Pro Gly Arg  
 263 1 5 10 15  
 264 Arg Leu Ala Ser Lys Asp Gly Leu Lys Leu Gly Thr Gly Val Lys Ala  
 265 20 25 30  
 266 Leu Asp Gly Lys Leu Gln Val Ser Thr Pro Arg Val Gly Lys Val Phe  
 267 35 40 45  
 268 Asn Ala Pro Ala Val Pro Lys Ala Ser Arg Lys Ala Leu Gly Thr Val  
 269 50 55 60  
 270 Asn Arg Val Ala Glu Lys Pro Met Lys Thr Gly Lys Pro Leu Gln Pro  
 271 65 70 75 80  
 272 Lys Gln Pro Thr Leu Thr Gly Lys Lys Ile Thr Glu Lys Ser Thr Lys  
 273 85 90 95  
 274 Thr Gln Ser Ser Val Pro Ala Pro Asp Asp Ala Tyr Pro Glu Ile Glu  
 275 100 105 110  
 276 Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Asp Leu Pro Glu Glu His  
 277 115 120 125  
 278 Gln Ile Ser Leu Leu Pro Leu Asn Gly Val Pro Leu Ile Thr Leu Asn  
 279 130 135 140  
 280 Glu Glu Arg Gly Leu Glu Lys Leu Leu His Leu Gly Pro Pro Ser Pro  
 281 145 150 155 160  
 282 Leu Lys Thr Pro Phe Leu Ser Trp Glu Ser Asp Pro Lys Pro Pro Ser  
 283 165 170 175  
 284 Ala Leu Ser Thr Leu Asp Val Glu Leu Pro Pro Val Cys Tyr Asp Ala  
 285 180 185 190  
 286 Asp Ile  
 290 <210> SEQ ID NO: 15  
 291 <211> LENGTH: 945  
 292 <212> TYPE: DNA  
 293 <213> ORGANISM: Mus musculus  
 295 <400> SEQUENCE: 15  
 296 tcttgaactt gttatgtagc aggaggccaa atttgagcat cctcttggtc tctctttata 60  
 297 gcagagattg taggctggag acagttttga tgggtgccaa cataaactga tttctgtaag 120  
 298 agttgagtggt tttatgaccg tggcgtgcag atttaggacg tggattaagc ctgttgactt 180  
 299 ctccagctac ttataaattt ttgtgcatag gtgccctggg taaagcttgg tctctgttac 240  
 300 tgcgtagttt ttccagccgt ctcaatgccca atattcaggc tctctccctt agagtaatcc 300  
 301 agaatggcta ctcttatctt tgttgataag gataatgaag aaccgggccg ccgtttgcca 360  
 302 tctaaggatg gtttgaagct gggcactggg gtcaaggcct tagatgggaa attgcaggtt 420  
 303 tcaacgcctc gagtcggcaa agtgttcaat gctccagccg tgcctaaagc cagcagaaag 480

## VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

Output Set: C:\CRF3\06012001\I854326.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:254 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13  
L:254 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13  
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13